

**Amendments to the Specification**

Kindly replace the paragraph beginning at page 7, line 28, with the following amended paragraph:

**Figure 2** depicts a graphical representation of a process by which genomic information, (for example SEQ ID NO: 1) can be processed (Figure 2A) and an example thereof (Figure 2B).

Kindly replace the paragraph beginning at page 7, line 30, with the following amended paragraph:

**Figure 3** depicts a graphical representation of a process by which processed genomic information (for example SEQ ID NO: 1) can be reconstructed (Figure 3A), and an example thereof (Figure 3B).

Kindly replace the paragraph beginning on page 15, line 14, with the following amended paragraph:

The function of the splitting algorithm is to randomise a sequence and generate information that can later be used to unrandomise the sequence. The randomisation is to be done in such a way that the resulting nucleotide sequence information becomes uninformative. The following sections describe one of the many algorithms that could be employed to perform the splitting, and are graphically represented in Figure 2 for the exemplary sequence of SEQ ID NO: 1.

Kindly replace the paragraph beginning on page 16, line 16, with the following amended paragraph:

The function of the reconstruction algorithm is to use the key generated in the splitting algorithm to unrandomise the sequence (Figure 3A). The following algorithm is one example of how a reconstruction algorithm is implemented. The nucleotide sequence of a gene (SEQ ID NO: 1) is reconstructed as follows with reference to Figure 3B.